



SEQUENCE LISTING

#5

<110> Sauter, Margret M.
Lorbiecke, Rene

<120> ALTERATION OF GROWTH AND ADAPTATION UNDER HYPOXIC
CONDITIONS

<130> CropDesign

<140>

<141>

<160> 18

<170> PatentIn Ver. 2.1

<210> 1

<211> 872

<212> DNA

<213> Rice

<220>

<221> CDS

<222> (69)..(668)

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Met Glu Asn Glu Phe Gln Asp Gly Lys Thr Glu Val Ile Glu
1 5 10

gca tgg tac atg gat gat agc gaa gag gac cag agg ctt cct cat cac 158
Ala Trp Tyr Met Asp Asp Ser Glu Glu Asp Gln Arg Leu Pro His His
15 20 25 30

cgc gaa ccc aaa gaa ttc att cct gtt gat aag ctt aca gaa cta gga 206
Arg Glu Pro Lys Glu Phe Ile Pro Val Asp Lys Leu Thr Glu Leu Gly
35 40 45

gta atc agc tgg cgc cta aat cct gat aac tgg gag aat tgc gag aac 254
Val Ile Ser Trp Arg Leu Asn Pro Asp Asn Trp Glu Asn Cys Glu Asn
50 55 60

ctg aag aga atc cgc gaa gcc aga ggt tac tct tat gtg gac att tgt 302
Leu Lys Arg Ile Arg Glu Ala Arg Gly Tyr Ser Tyr Val Asp Ile Cys
65 70 75

gat	gtg	tgc	cca	gag	aag	ctg	cca	aat	tat	gaa	act	aag	atc	aag	agt	350
Asp	Val	Cys	Pro	Glu	Lys	Leu	Pro	Asn	Tyr	Glu	Thr	Lys	Ile	Lys	Ser	
	80					85					90					
ttc	ttt	gaa	gaa	cac	ctg	cat	acc	gat	gaa	gaa	ata	cgc	tat	tgt	ctt	398
Phe	Phe	Glu	Glu	His	Leu	His	Thr	Asp	Glu	Glu	Ile	Arg	Tyr	Cys	Leu	
	95				100					105					110	
gaa	ggg	agt	gga	tac	ttt	gat	gtg	aga	gac	caa	aat	gat	cag	tgg	att	446
Glu	Gly	Ser	Gly	Tyr	Phe	Asp	Val	Arg	Asp	Gln	Asn	Asp	Gln	Trp	Ile	
				115					120					125		
cgt	ata	gca	ctg	aag	aaa	gga	ggc	atg	att	gtt	ctg	cct	gca	ggg	atg	494
Arg	Ile	Ala	Leu	Lys	Lys	Gly	Gly	Met	Ile	Val	Leu	Pro	Ala	Gly	Met	
			130					135					140			
tac	cac	cgc	ttt	acg	ttg	gac	acc	gac	aac	tat	atc	aag	gca	atg	cga	542
Tyr	His	Arg	Phe	Thr	Leu	Asp	Thr	Asp	Asn	Tyr	Ile	Lys	Ala	Met	Arg	
		145					150					155				
ctg	ttt	gtt	ggc	gat	cct	gtt	tgg	aca	ccc	tac	aac	cgt	ccc	cat	gac	590
Leu	Phe	Val	Gly	Asp	Pro	Val	Trp	Thr	Pro	Tyr	Asn	Arg	Pro	His	Asp	
	160					165					170					
cat	ctt	cct	gca	aga	aag	gag	ttt	ttg	gct	aaa	ctt	ctc	aag	tca	gaa	638
His	Leu	Pro	Ala	Arg	Lys	Glu	Phe	Leu	Ala	Lys	Leu	Leu	Lys	Ser	Glu	
	175				180					185					190	
ggg	gaa	aat	caa	gca	gtt	gaa	ggc	ttc	tga	ggg	ttt	gtt	ggg	ctc	ctg	688
Gly	Glu	Asn	Gln	Ala	Val	Glu	Gly	Phe								
			195					200								
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ggctatgggc gccactcacc aacttgaagt gaaagattta atgatttttg ttaattctta																808
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<210> 2

<211> 199

<212> PRT

<213> Rice

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Pro	Lys	Glu	Phe	Ile	Pro	Val	Asp	Lys	Leu	Thr	Glu	Leu	Gly	Val	Ile
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Ser	Trp	Arg	Leu	Asn	Pro	Asp	Asn	Trp	Glu	Asn	Cys	Glu	Asn	Leu	Lys
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Arg	Ile	Arg	Glu	Ala	Arg	Gly	Tyr	Ser	Tyr	Val	Asp	Ile	Cys	Asp	Val
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Cys	Pro	Glu	Lys	Leu	Pro	Asn	Tyr	Glu	Thr	Lys	Ile	Lys	Ser	Phe	Phe
				85					90					95	
Glu	Glu	His	Leu	His	Thr	Asp	Glu	Glu	Ile	Arg	Tyr	Cys	Leu	Glu	Gly
			100					105					110		
Ser	Gly	Tyr	Phe	Asp	Val	Arg	Asp	Gln	Asn	Asp	Gln	Trp	Ile	Arg	Ile
	115						120					125			
Ala	Leu	Lys	Lys	Gly	Gly	Met	Ile	Val	Leu	Pro	Ala	Gly	Met	Tyr	His
	130					135					140				
Arg	Phe	Thr	Leu	Asp	Thr	Asp	Asn	Tyr	Ile	Lys	Ala	Met	Arg	Leu	Phe
145					150					155					160
Val	Gly	Asp	Pro	Val	Trp	Thr	Pro	Tyr	Asn	Arg	Pro	His	Asp	His	Leu
				165					170					175	
Pro	Ala	Arg	Lys	Glu	Phe	Leu	Ala	Lys	Leu	Leu	Lys	Ser	Glu	Gly	Glu
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<213> Rice

<220>

<221> CDS

<222> (139)..(735)

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aggctatccg gaatcgggag ggtttcccaa taggaaagca actcaggact caggagcggc 120

gtctgagagg tttcagag atg gag aac cag ttc cag gat ggc aag gag gag 171

Met Glu Asn Gln Phe Gln Asp Gly Lys Glu Glu

1

5

10

gtc atc gaa gct tgg tac atg gat gac agt gaa gag gac cag agg ctt 219

Val Ile Glu Ala Trp Tyr Met Asp Asp Ser Glu Glu Asp Gln Arg Leu

15

20

25

cct cat cat cgt gag ccc aaa gaa ttc att cct ctt agc aaa ctt tca	267
Pro His His Arg Glu Pro Lys Glu Phe Ile Pro Leu Ser Lys Leu Ser	
30 35 40	
gag tta gga ata tta agc tgg cgc ctg aat gct gat gac tgg gag aat	315
Glu Leu Gly Ile Leu Ser Trp Arg Leu Asn Ala Asp Asp Trp Glu Asn	
45 50 55	
gat gag aac ctc aag aaa atc cgt gag gcc agg gga tac tct tac atg	363
Asp Glu Asn Leu Lys Lys Ile Arg Glu Ala Arg Gly Tyr Ser Tyr Met	
60 65 70 75	
gat att tgt gat gtg tgt cca gaa aag ctg cca aac tat gag gct aag	411
Asp Ile Cys Asp Val Cys Pro Glu Lys Leu Pro Asn Tyr Glu Ala Lys	
80 85 90	
ctg aaa aat ttc ttt gaa gaa cac ttg cat act gat gaa gag ata cgc	459
Leu Lys Asn Phe Phe Glu Glu His Leu His Thr Asp Glu Glu Ile Arg	
95 100 105	
tat tgt ctt gag gga agt gga tac ttc gat gtc agg gac caa aat gat	507
Tyr Cys Leu Glu Gly Ser Gly Tyr Phe Asp Val Arg Asp Gln Asn Asp	
110 115 120	
cag tgg atc cgt gta gca gtg aag aaa ggg ggc atg att gtt ttg cct	555
Gln Trp Ile Arg Val Ala Val Lys Lys Gly Gly Met Ile Val Leu Pro	
125 130 135	
gcg gga atg tat cac cgc ttc aca ttg gac agt gac aac tac atc aag	603
Ala Gly Met Tyr His Arg Phe Thr Leu Asp Ser Asp Asn Tyr Ile Lys	
140 145 150 155	
gca atg cgg ctc ttt gtg gga gag cct gtc tgg acg ccg tac aac cgt	651
Ala Met Arg Leu Phe Val Gly Glu Pro Val Trp Thr Pro Tyr Asn Arg	
160 165 170	
ccc cat gac cat ctg cca gct aga aag gag tat gtc gaa aaa att atc	699
Pro His Asp His Leu Pro Ala Arg Lys Glu Tyr Val Glu Lys Ile Ile	
175 180 185	
aac agg ggt gga act caa gct gtc gaa gct cgt taa aggcataatca	745
Asn Arg Gly Gly Thr Gln Ala Val Glu Ala Arg	
190 195	
agatgtgctt cctagttcgg tggtctgtta cactctacag atactgaata aactgtgcta	805
tcagctgttg caatgggctc ctaccgacat cttacatcat ttggcagtat tttgcacaaa	865

cccgccttaaa atctccctga aaatacgcac gtcaccatgt cagagtgttt atatacaata 925
atgacacttc agtccacagt cagcaaggga ctaatgacaa aaaaaaaaaa aaaaa 980

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<213> Rice

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Pro Lys Glu Phe Ile Pro Leu Ser Lys Leu Ser Glu Leu Gly Ile Leu
35 40 45
Ser Trp Arg Leu Asn Ala Asp Asp Trp Glu Asn Asp Glu Asn Leu Lys
50 55 60
Lys Ile Arg Glu Ala Arg Gly Tyr Ser Tyr Met Asp Ile Cys Asp Val
65 70 75 80
Cys Pro Glu Lys Leu Pro Asn Tyr Glu Ala Lys Leu Lys Asn Phe Phe
85 90 95
Glu Glu His Leu His Thr Asp Glu Glu Ile Arg Tyr Cys Leu Glu Gly
100 105 110
Ser Gly Tyr Phe Asp Val Arg Asp Gln Asn Asp Gln Trp Ile Arg Val
115 120 125
Ala Val Lys Lys Gly Gly Met Ile Val Leu Pro Ala Gly Met Tyr His
130 135 140
Arg Phe Thr Leu Asp Ser Asp Asn Tyr Ile Lys Ala Met Arg Leu Phe
145 150 155 160
Val Gly Glu Pro Val Trp Thr Pro Tyr Asn Arg Pro His Asp His Leu
165 170 175
Pro Ala Arg Lys Glu Tyr Val Glu Lys Ile Ile Asn Arg Gly Gly Thr
180 185 190
Gln Ala Val Glu Ala Arg
195

<210> 5
<211> 774
<212> DNA
<213> Tomato

<220>
<221> CDS
<222> (1) .. (591)

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Ala Pro Asp Pro Arg Glu Asp Val Ile Gln Ala Trp Tyr Met Asp Asp
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aac gat gag gac cag agg ctt cct cat cac cgt gag cca aag gaa ttt 96
Asn Asp Glu Asp Gln Arg Leu Pro His His Arg Glu Pro Lys Glu Phe
20 25 30

gtg tct ctt gac aag ctg gct gaa ctt gga gtg ctc agc tgg aga ctt 144
Val Ser Leu Asp Lys Leu Ala Glu Leu Gly Val Leu Ser Trp Arg Leu
35 40 45

gat gct gac aat tat gag act gat gag gag ttg aag aaa att cgg gaa 192
Asp Ala Asp Asn Tyr Glu Thr Asp Glu Glu Leu Lys Lys Ile Arg Glu
50 55 60

gat cgt gga tat tca tac att gat ttc tgt gag gtt tgc cct gag aaa 240
Asp Arg Gly Tyr Ser Tyr Ile Asp Phe Cys Glu Val Cys Pro Glu Lys
65 70 75 80

cta ccg aat tac gag gag aaa atc aag aac ttt ttt gaa gaa cac ctg 288
Leu Pro Asn Tyr Glu Glu Lys Ile Lys Asn Phe Phe Glu Glu His Leu
85 90 95

cac acc gac gag gag atc cgt tac gct gtt gca gga agt ggt tac ttt 336
His Thr Asp Glu Glu Ile Arg Tyr Ala Val Ala Gly Ser Gly Tyr Phe
100 105 110

gat gtc cgc gat gtg aat gag agc tgg att cgc gtc tgg gta aag aaa 384
Asp Val Arg Asp Val Asn Glu Ser Trp Ile Arg Val Trp Val Lys Lys
115 120 125

ggt gga atg att gtt ctt cct gct gga atc tat cac cgc ttc acg ctt 432
Gly Gly Met Ile Val Leu Pro Ala Gly Ile Tyr His Arg Phe Thr Leu
130 135 140

gat tca agc aac tac att aag gca atg cgt ctc ttt gtt ggt gac cca 480
Asp Ser Ser Asn Tyr Ile Lys Ala Met Arg Leu Phe Val Gly Asp Pro
145 150 155 160

att tgg act cca tac aat cgt cca cat gat cat ctt ccc gca agg caa 528
Ile Trp Thr Pro Tyr Asn Arg Pro His Asp His Leu Pro Ala Arg Gln
165 170 175

gaa tat gtt gag acg ttt gtc aac gca gat ggc gct ggt cgt gct gtt 576
Glu Tyr Val Glu Thr Phe Val Asn Ala Asp Gly Ala Gly Arg Ala Val
180 185 190

aat gct gct gct taa atcaactata ggagaggaat ttgaaatcgt actagattgt 631
Asn Ala Ala Ala
195

aataaatatt accatatgggt ggctttgctg ttcttgatgt gtgccttact aagcatgttt 691
aatgttgat tgtggcacta aataaatcac cccctatggg agattgattg tttatatgca 751
agtgaatttt attatgtgat ttt 774

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<212> PRT
<213> Tomato

<400> 6
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Asn Asp Glu Asp Gln Arg Leu Pro His His Arg Glu Pro Lys Glu Phe
20 25 30
Val Ser Leu Asp Lys Leu Ala Glu Leu Gly Val Leu Ser Trp Arg Leu
35 40 45
Asp Ala Asp Asn Tyr Glu Thr Asp Glu Glu Leu Lys Lys Ile Arg Glu
50 55 60
Asp Arg Gly Tyr Ser Tyr Ile Asp Phe Cys Glu Val Cys Pro Glu Lys
65 70 75 80
Leu Pro Asn Tyr Glu Lys Ile Lys Asn Phe Phe Glu Glu His Leu
85 90 95
His Thr Asp Glu Glu Ile Arg Tyr Ala Val Ala Gly Ser Gly Tyr Phe
100 105 110
Asp Val Arg Asp Val Asn Glu Ser Trp Ile Arg Val Trp Val Lys Lys
115 120 125
Gly Gly Met Ile Val Leu Pro Ala Gly Ile Tyr His Arg Phe Thr Leu
130 135 140
Asp Ser Ser Asn Tyr Ile Lys Ala Met Arg Leu Phe Val Gly Asp Pro
145 150 155 160
Ile Trp Thr Pro Tyr Asn Arg Pro His Asp His Leu Pro Ala Arg Gln
165 170 175
Glu Tyr Val Glu Thr Phe Val Asn Ala Asp Gly Ala Gly Arg Ala Val
180 185 190
Asn Ala Ala Ala
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<210> 7
<211> 603
<212> DNA

<213> Tomato

<220>

<221> CDS

<222> (3)..(572)

<400> 7

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gat cag cgg cta ccg cac cag aag aac cca ccg gag ttt gtt tca gtg	95
Asp Gln Arg Leu Pro His Gln Lys Asn Pro Pro Glu Phe Val Ser Val	
20 25 30	
gag aaa tta gca gta atc gga gtt tta tac tgg aaa ttg aac cct aat	143
Glu Lys Leu Ala Val Ile Gly Val Leu Tyr Trp Lys Leu Asn Pro Asn	
35 40 45	
gat tac gag aac gat gaa gaa ttg aaa aaa att cgt caa agt aga ggc	191
Asp Tyr Glu Asn Asp Glu Glu Leu Lys Lys Ile Arg Gln Ser Arg Gly	
50 55 60	
tac agc tac atg gac ttg ctg gat ttg tgc cct gag aag gtg gat aac	239
Tyr Ser Tyr Met Asp Leu Leu Asp Leu Cys Pro Glu Lys Val Asp Asn	
65 70 75	
tat gag cag aag ttg aaa aat ttc tat acg gag cac ata cac gca gat	287
Tyr Glu Gln Lys Leu Lys Asn Phe Tyr Thr Glu His Ile His Ala Asp	
80 85 90 95	
gag gag ata cgt tac tgt ctg gaa ggg agt gga tat ttt gat gtg aga	335
Glu Glu Ile Arg Tyr Cys Leu Glu Gly Ser Gly Tyr Phe Asp Val Arg	
100 105 110	
gac aag gat gat cgc tgg att cgc atc tgg atg aag gcc ggt gat atg	383
Asp Lys Asp Asp Arg Trp Ile Arg Ile Trp Met Lys Ala Gly Asp Met	
115 120 125	
att gtc ttg cct gct ggg att tac cac cgg ttc acc cta gat act gat	431
Ile Val Leu Pro Ala Gly Ile Tyr His Arg Phe Thr Leu Asp Thr Asp	
130 135 140	
aac tat gtc aag ttg atg agg ttg ttt gtg gga gag ccg gtg tgg acg	479
Asn Tyr Val Lys Leu Met Arg Leu Phe Val Gly Glu Pro Val Trp Thr	
145 150 155	
cct tac aat cga cca caa gaa gat cat cca gca agg aag gag tac atc	527
Pro Tyr Asn Arg Pro Gln Glu Asp His Pro Ala Arg Lys Glu Tyr Ile	
160 165 170 175	

aag agt gtt act gaa aga gta gga gtg cct ctt aca gca cac taa 572
Lys Ser Val Thr Glu Arg Val Gly Val Pro Leu Thr Ala His
180 185 190

gacatatttg agctttacaa acctgagagt g 603

<210> 8
<211> 189
<212> PRT
<213> Tomato

<400> 8
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Gln Arg Leu Pro His Gln Lys Asn Pro Pro Glu Phe Val Ser Val Glu
20 25 30
Lys Leu Ala Val Ile Gly Val Leu Tyr Trp Lys Leu Asn Pro Asn Asp
35 40 45
Tyr Glu Asn Asp Glu Glu Leu Lys Lys Ile Arg Gln Ser Arg Gly Tyr
50 55 60
Ser Tyr Met Asp Leu Leu Asp Leu Cys Pro Glu Lys Val Asp Asn Tyr
65 70 75 80
Glu Gln Lys Leu Lys Asn Phe Tyr Thr Glu His Ile His Ala Asp Glu
85 90 95
Glu Ile Arg Tyr Cys Leu Glu Gly Ser Gly Tyr Phe Asp Val Arg Asp
100 105 110
Lys Asp Asp Arg Trp Ile Arg Ile Trp Met Lys Ala Gly Asp Met Ile
115 120 125
Val Leu Pro Ala Gly Ile Tyr His Arg Phe Thr Leu Asp Thr Asp Asn
130 135 140
Tyr Val Lys Leu Met Arg Leu Phe Val Gly Glu Pro Val Trp Thr Pro
145 150 155 160
Tyr Asn Arg Pro Gln Glu Asp His Pro Ala Arg Lys Glu Tyr Ile Lys
165 170 175
Ser Val Thr Glu Arg Val Gly Val Pro Leu Thr Ala His
180 185

<210> 9
<211> 889
<212> DNA
<213> Soybean

<220>
<221> CDS
<222> (32) .. (634)

<400> 9

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cca cga gag gat gtc ctt caa gcc tgg tac atg gat gat agt gat gaa	100
Pro Arg Glu Asp Val Leu Gln Ala Trp Tyr Met Asp Asp Ser Asp Glu	
10 15 20	
gat caa aga ctc ccc cac cac aaa gaa ccc aag gag ttt gtc tcg ttg	148
Asp Gln Arg Leu Pro His His Lys Glu Pro Lys Glu Phe Val Ser Leu	
25 30 35	
gac caa ctt gct gaa ctt gga gtc ctt agc tgg aaa cta gat gct gat	196
Asp Gln Leu Ala Glu Leu Gly Val Leu Ser Trp Lys Leu Asp Ala Asp	
40 45 50 55	
aac cat gaa aat gat cca gag ctg aag aag att cgt gaa gag cgt ggt	244
Asn His Glu Asn Asp Pro Glu Leu Lys Lys Ile Arg Glu Glu Arg Gly	
60 65 70	
tac acc tac atg gat gtt tgt gag gtc tgc cca gaa aag ttg cca aat	292
Tyr Thr Tyr Met Asp Val Cys Glu Val Cys Pro Glu Lys Leu Pro Asn	
75 80 85	
tat gaa cag aaa atc aaa agc ttc ttt gaa gag cat ctt cac act gat	340
Tyr Glu Gln Lys Ile Lys Ser Phe Phe Glu Glu His Leu His Thr Asp	
90 95 100	
gag gag atc cgc ttt tgt gct gct gga agt ggc tat ttt gat gtt agg	388
Glu Glu Ile Arg Phe Cys Ala Ala Gly Ser Gly Tyr Phe Asp Val Arg	
105 110 115	
gat cgc aat gaa gct tgg att cgt gtg tgg gtc aag aaa gga gga atg	436
Asp Arg Asn Glu Ala Trp Ile Arg Val Trp Val Lys Lys Gly Gly Met	
120 125 130 135	
atc atc tta cct gcc gga att tat cat cgc ttt acg cta gat gag agc	484
Ile Ile Leu Pro Ala Gly Ile Tyr His Arg Phe Thr Leu Asp Glu Ser	
140 145 150	
aac tac att aag gct ttg cgt ttt ttt gtt ggt gag cca gtt tgg act	532
Asn Tyr Ile Lys Ala Leu Arg Phe Phe Val Gly Glu Pro Val Trp Thr	
155 160 165	
cca tac aat cgt cca aat gac cat ctc cct gca aga caa caa tat gtc	580
Pro Tyr Asn Arg Pro Asn Asp His Leu Pro Ala Arg Gln Gln Tyr Val	
170 175 180	

aag gat ttt gtg gaa aag gat gtt agc agc cat gct gtt gat gcc acc 628
 Lys Asp Phe Val Glu Lys Asp Val Ser Ser His Ala Val Asp Ala Thr
 185 190 195

gcg taa gatctgggttc tgcctaataca tagtaccaca tgaaaaggac caagactttg 684
 Ala
 200

ttgctaaagt aagggtttgaa aaaaagaaaa taatgggtgtc tttaaataaa gggtcctggc 744
 ttgttatgcc ttgatgtacc ctgcgcagtg tttttgttgc ctgtccctgt ataaagattg 804
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<210> 10
 <211> 200
 <212> PRT
 <213> Soybean

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 Asp Pro Arg Glu Asp Val Leu Gln Ala Trp Tyr Met Asp Asp Ser Asp
 20 25 30
 Glu Asp Gln Arg Leu Pro His His Lys Glu Pro Lys Glu Phe Val Ser
 35 40 45
 Leu Asp Gln Leu Ala Glu Leu Gly Val Leu Ser Trp Lys Leu Asp Ala
 50 55 60
 Asp Asn His Glu Asn Asp Pro Glu Leu Lys Lys Ile Arg Glu Glu Arg
 65 70 75 80
 Gly Tyr Thr Tyr Met Asp Val Cys Glu Val Cys Pro Glu Lys Leu Pro
 85 90 95
 Asn Tyr Glu Gln Lys Ile Lys Ser Phe Phe Glu Glu His Leu His Thr
 100 105 110
 Asp Glu Glu Ile Arg Phe Cys Ala Ala Gly Ser Gly Tyr Phe Asp Val
 115 120 125
 Arg Asp Arg Asn Glu Ala Trp Ile Arg Val Trp Val Lys Lys Gly Gly
 130 135 140
 Met Ile Ile Leu Pro Ala Gly Ile Tyr His Arg Phe Thr Leu Asp Glu
 145 150 155 160
 Ser Asn Tyr Ile Lys Ala Leu Arg Phe Phe Val Gly Glu Pro Val Trp
 165 170 175
 Thr Pro Tyr Asn Arg Pro Asn Asp His Leu Pro Ala Arg Gln Gln Tyr
 180 185 190

Val Lys Asp Phe Val Glu Lys Asp Val Ser Ser His Ala Val Asp Ala
 195 200 205
 Thr Ala
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<210> 11
 <211> 933
 <212> DNA
 <213> Cotton

<220>
 <221> CDS
 <222> (33)..(635)

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 Lys Arg Glu Glu Val Ile Gln Ala Trp Tyr Met Asp Asp Ser Asp Glu
 10 15 20
 gat cag agg ctt cct cat cac cgt gaa cct aag gaa tat gta tcc ttg 149
 Asp Gln Arg Leu Pro His His Arg Glu Pro Lys Glu Tyr Val Ser Leu
 25 30 35
 gat aaa ctt gct gag ctt gga gta ctc agc tgg cga ttg gat gct gat 197
 Asp Lys Leu Ala Glu Leu Gly Val Leu Ser Trp Arg Leu Asp Ala Asp
 40 45 50 55
 aac tat gaa aat gat gaa gag ttg aag aaa att cgt gaa gaa cga ggt 245
 Asn Tyr Glu Asn Asp Glu Glu Leu Lys Lys Ile Arg Glu Glu Arg Gly
 60 65 70
 tac tcc tac atg gac ttc tgc gag gtt tgc cct gag aag ctt cca aat 293
 Tyr Ser Tyr Met Asp Phe Cys Glu Val Cys Pro Glu Lys Leu Pro Asn
 75 80 85
 tat gag gag aag ata aaa aat ttc ttc gaa gaa cat att cat act gat 341
 Tyr Glu Glu Lys Ile Lys Asn Phe Phe Glu Glu His Ile His Thr Asp
 90 95 100
 gag gag atc cgt tac tgt gtg gca gga agt ggt tat ttt gat gta cgg 389
 Glu Glu Ile Arg Tyr Cys Val Ala Gly Ser Gly Tyr Phe Asp Val Arg
 105 110 115

gat cat aat gat aaa tgg att cgt gtg tgg gtg aag aaa gga ggc atg 437
 Asp His Asn Asp Lys Trp Ile Arg Val Trp Val Lys Lys Gly Gly Met
 120 125 130 135

ata gtt tta cct gct gga att tat cat cgc ttt act ctg gat aca gac 485
 Ile Val Leu Pro Ala Gly Ile Tyr His Arg Phe Thr Leu Asp Thr Asp
 140 145 150

aac tat att aag gca atg cgg ctc ttt gtt ggt gat cca att tgg act 533
 Asn Tyr Ile Lys Ala Met Arg Leu Phe Val Gly Asp Pro Ile Trp Thr
 155 160 165

ccg tac aat cgt ccg cac gat cat ctt cct gca agg aag gag tat atc 581
 Pro Tyr Asn Arg Pro His Asp His Leu Pro Ala Arg Lys Glu Tyr Ile
 170 175 180

aag aac ttt ttg cgg gag gaa ggt ggt ggc caa gcc gtt gat gct gcc 629
 Lys Asn Phe Leu Arg Glu Glu Gly Gly Gly Gln Ala Val Asp Ala Ala
 185 190 195

gca taa aatcaacatt catctggtgg tggccaagtc gttgatgctg ccgcataaaa 685
 Ala
 200

tcagcattca tctctggtat cgtgtcttat aaaatatgaa accccggatt tgtggtaata 745

aataagtcta ggcttgtctg cttttgatgc gtggatatgg atcgttatgg ttgttgcttg 805

ctatatattg cctattccat atcgaaaatt cgcaaacttg ctatgtatctt ctacatttta 865

tgtgcttact accagattgg ctcttaataa tcaaagttta cataatatac atttcgctcga 925

cgcggccg 933

<210> 12

<211> 200

<212> PRT

<213> Cotton

<400> 12

Met Thr Met Gly Ser Ala Asp Lys Arg Glu Glu Val Ile Gln Ala Trp
 1 5 10 15
 Tyr Met Asp Asp Ser Asp Glu Asp Gln Arg Leu Pro His His Arg Glu
 20 25 30
 Pro Lys Glu Tyr Val Ser Leu Asp Lys Leu Ala Glu Leu Gly Val Leu
 35 40 45
 Ser Trp Arg Leu Asp Ala Asp Asn Tyr Glu Asn Asp Glu Glu Leu Lys
 50 55 60

Lys	Ile	Arg	Glu	Glu	Arg	Gly	Tyr	Ser	Tyr	Met	Asp	Phe	Cys	Glu	Val	
65					70					75					80	
Cys	Pro	Glu	Lys	Leu	Pro	Asn	Tyr	Glu	Glu	Lys	Ile	Lys	Asn	Phe	Phe	
			85						90					95		
Glu	Glu	His	Ile	His	Thr	Asp	Glu	Glu	Ile	Arg	Tyr	Cys	Val	Ala	Gly	
		100					105					110				
Ser	Gly	Tyr	Phe	Asp	Val	Arg	Asp	His	Asn	Asp	Lys	Trp	Ile	Arg	Val	
	115					120					125					
Trp	Val	Lys	Lys	Gly	Gly	Met	Ile	Val	Leu	Pro	Ala	Gly	Ile	Tyr	His	
	130					135					140					
Arg	Phe	Thr	Leu	Asp	Thr	Asp	Asn	Tyr	Ile	Lys	Ala	Met	Arg	Leu	Phe	
145					150					155					160	
Val	Gly	Asp	Pro	Ile	Trp	Thr	Pro	Tyr	Asn	Arg	Pro	His	Asp	His	Leu	
			165						170					175		
Pro	Ala	Arg	Lys	Glu	Tyr	Ile	Lys	Asn	Phe	Leu	Arg	Glu	Glu	Gly	Gly	
		180						185					190			
Gly	Gln	Ala	Val	Asp	Ala	Ala	Ala									
	195						200									

<210> 13
 <211> 919
 <212> DNA
 <213> Human

<220>
 <221> CDS
 <222> (1)..(564)

<400> 13																
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Arg	Thr	Arg	His	Pro	His	Cys	Ala	Ser	Val	Val	Gln	Ala	Trp	Tyr	Met	
1				5					10					15		
gac	gac	gcc	ccg	ggc	acc	cgc	ggc	aac	ccc	acc	gcc	ccg	acc	ccg	gcc	96
Asp	Asp	Ala	Pro	Gly	Thr	Arg	Gly	Asn	Pro	Thr	Ala	Pro	Thr	Pro	Ala	
			20					25					30			
gcc	cag	tgc	gct	gga	gca	gct	gcg	cgg	ctc	ggg	gtg	ctc	tac	tgg	aag	144
Ala	Gln	Cys	Ala	Gly	Ala	Ala	Ala	Arg	Leu	Gly	Val	Leu	Tyr	Trp	Lys	
		35					40					45				
ctg	gat	gct	gac	aaa	tat	gag	aat	gat	cca	gaa	tta	gaa	aag	atc	cga	192
Leu	Asp	Ala	Asp	Lys	Tyr	Glu	Asn	Asp	Pro	Glu	Leu	Glu	Lys	Ile	Arg	
	50					55					60					
aga	gag	agg	aac	tac	tcc	tgg	atg	gac	atc	ata	acc	ata	tgc	aaa	gat	240
Arg	Glu	Arg	Asn	Tyr	Ser	Trp	Met	Asp	Ile	Ile	Thr	Ile	Cys	Lys	Asp	
65					70				75						80	

aaa cta cca aat tat gaa gaa aag att aag atg ttc tac gag gag cat	288
Lys Leu Pro Asn Tyr Glu Glu Lys Ile Lys Met Phe Tyr Glu Glu His	
85 90 95	
ttg cac ttg gac gat gag atc cgc tac atc ctg gat ggc agt ggg tac	336
Leu His Leu Asp Asp Glu Ile Arg Tyr Ile Leu Asp Gly Ser Gly Tyr	
100 105 110	
ttc gat gtg agg gac aag gag gac cag tgg atc cgg atc ttc atg gag	384
Phe Asp Val Arg Asp Lys Glu Asp Gln Trp Ile Arg Ile Phe Met Glu	
115 120 125	
aag gga gac atg gtg acg ctc ccc gcg ggg atc tat cac cgc ttc acg	432
Lys Gly Asp Met Val Thr Leu Pro Ala Gly Ile Tyr His Arg Phe Thr	
130 135 140	
gtg gac gag aag aac tac acg aag gcc atg cgg ctg ttt gtg gga gaa	480
Val Asp Glu Lys Asn Tyr Thr Lys Ala Met Arg Leu Phe Val Gly Glu	
145 150 155 160	
ccg gtg tgg aca gcg tac aac cgg ccc gct gac cat ttt gaa gcc cgc	528
Pro Val Trp Thr Ala Tyr Asn Arg Pro Ala Asp His Phe Glu Ala Arg	
165 170 175	
ggg cag tac gtg aaa ttt ctg gca cag acc gcc tag cagtgtgcc	574
Gly Gln Tyr Val Lys Phe Leu Ala Gln Thr Ala	
180 185	
tggaactaa cacgtgcctc gtaaagggtcc ccaatgtaat gaactgagca gaaaattcaa	634
tcaactttct ctttgctttt agaggatagc cttgaggtag attatctttc ctttgtaaga	694
ttatttgatc agaataatttt gtaatgaaag gatctagaaa gcaacttgga agtgtaaaga	754
gtcaccttca ttttctgtaa ctcaatcaag actgggtgggt ccatggccct gtgttagttc	814
attgcattca ggttgagtcc caaatgaaag tttcatctcc cgaaatgcag ttccttagat	874
gcccattctgg acgtgaatgc cgcgcctgcg tgtaagaagg tgcaat	920

<210> 14

<211> 187

<212> PRT

<213> Human

<400> 14

Arg	Thr	Arg	His	Pro	His	Cys	Ala	Ser	Val	Val	Gln	Ala	Trp	Tyr	Met
1				5					10					15	
Asp	Asp	Ala	Pro	Gly	Thr	Arg	Gly	Asn	Pro	Thr	Ala	Pro	Thr	Pro	Ala
			20					25					30		
Ala	Gln	Cys	Ala	Gly	Ala	Ala	Ala	Arg	Leu	Gly	Val	Leu	Tyr	Trp	Lys
		35					40					45			
Leu	Asp	Ala	Asp	Lys	Tyr	Glu	Asn	Asp	Pro	Glu	Leu	Glu	Lys	Ile	Arg
	50					55					60				
Arg	Glu	Arg	Asn	Tyr	Ser	Trp	Met	Asp	Ile	Ile	Thr	Ile	Cys	Lys	Asp
65					70					75					80
Lys	Leu	Pro	Asn	Tyr	Glu	Glu	Lys	Ile	Lys	Met	Phe	Tyr	Glu	Glu	His
				85					90					95	
Leu	His	Leu	Asp	Asp	Glu	Ile	Arg	Tyr	Ile	Leu	Asp	Gly	Ser	Gly	Tyr
			100					105					110		
Phe	Asp	Val	Arg	Asp	Lys	Glu	Asp	Gln	Trp	Ile	Arg	Ile	Phe	Met	Glu
		115					120					125			
Lys	Gly	Asp	Met	Val	Thr	Leu	Pro	Ala	Gly	Ile	Tyr	His	Arg	Phe	Thr
	130					135					140				
Val	Asp	Glu	Lys	Asn	Tyr	Thr	Lys	Ala	Met	Arg	Leu	Phe	Val	Gly	Glu
145					150					155					160
Pro	Val	Trp	Thr	Ala	Tyr	Asn	Arg	Pro	Ala	Asp	His	Phe	Glu	Ala	Arg
				165					170					175	
Gly	Gln	Tyr	Val	Lys	Phe	Leu	Ala	Gln	Thr	Ala					
			180					185							

<210> 15
 <211> 972
 <212> DNA
 <213> Mouse

<220>
 <221> CDS
 <222> (17) .. (556)

<400> 15
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 Met Val Gln Ala Trp Tyr Met Asp Glu Ser Thr Ala
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gac	ccg	cgg	aag	ccc	cac	cgc	gca	cag	ccc	gac	cgc	ccc	gtg	agc	ctg	100
Asp	Pro	Arg	Lys	Pro	His	Arg	Ala	Gln	Pro	Asp	Arg	Pro	Val	Ser	Leu	
		15					20				25					

gag	cag	ctg	cgc	acg	ctc	gga	gtg	ctc	tat	tgg	aag	cta	gat	gct	gac	148
Glu	Gln	Leu	Arg	Thr	Leu	Gly	Val	Leu	Tyr	Trp	Lys	Leu	Asp	Ala	Asp	
		30				35					40					

aag tat gag aac gat cca gaa cta gaa aag atc cgg aaa atg aga aac	196
Lys Tyr Glu Asn Asp Pro Glu Leu Glu Lys Ile Arg Lys Met Arg Asn	
45 50 55 60	
tac tcc tgg atg gac atc atc acc ata tgc aaa gat aca ctt ccc aat	244
Tyr Ser Trp Met Asp Ile Ile Thr Ile Cys Lys Asp Thr Leu Pro Asn	
65 70 75	
tac gag gag aag atc aag atg ttc ttt gag gaa cat ctg cat ctg gat	292
Tyr Glu Glu Lys Ile Lys Met Phe Phe Glu Glu His Leu His Leu Asp	
80 85 90	
gag gag atc cgc tac atc ctg gag ggt agt ggg tac ttc gat gtc agg	340
Glu Glu Ile Arg Tyr Ile Leu Glu Gly Ser Gly Tyr Phe Asp Val Arg	
95 100 105	
gac aag gag gac aag tgg atc cgg att tcc atg gag aag ggg gac atg	388
Asp Lys Glu Asp Lys Trp Ile Arg Ile Ser Met Glu Lys Gly Asp Met	
110 115 120	
att act ctt cct gcc ggc atc tat cac cgc ttc aca ctg gac gag aag	436
Ile Thr Leu Pro Ala Gly Ile Tyr His Arg Phe Thr Leu Asp Glu Lys	
125 130 135 140	
aat tac gtg aag gcc atg cgg ctg ttt gtt gga gaa cct gtg tgg aca	484
Asn Tyr Val Lys Ala Met Arg Leu Phe Val Gly Glu Pro Val Trp Thr	
145 150 155	
cca tac aac cgg cca gct gac cat ttt gat gcc cgt gta cag tac atg	532
Pro Tyr Asn Arg Pro Ala Asp His Phe Asp Ala Arg Val Gln Tyr Met	
160 165 170	
agt ttt ttg gaa gga aca gca tag cagtgtcct caaagagaaa actgcactgt	586
Ser Phe Leu Glu Gly Thr Ala	
175 180	
gtgaatctcc tgctgtggta accgaatgga aagttgctca cttttctgct tttgtatttg	646
aacttgaggc tagactagct ctctttgcta ggattgtgag atcagtgtct tttaaataa	706
agcctctcta aaagtgagtt ttacatggaa gccacaaaaa tgtgaaaaag tgaccttaat	766
tttccctaac tgtcaagact tagaggtata ggagccctgg attggtatgt gcattcatgc	826
atggccaatc ttcattctccc agatcttttag gtgtctgttg gtgtgaagct atgcctcctg	886
caagagggca gttataacca gcacaactaa ccagatgacg tttttctcct ttgctgattg	946
ttgagtgggg aagtgggggtt gttggt	972

<210> 16
 <211> 179
 <212> PRT
 <213> Mouse

<400> 16
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 Ala Asp Pro Arg Lys Pro His Arg Ala Gln Pro Asp Arg Pro Val Ser
 20 25 30
 Leu Glu Gln Leu Arg Thr Leu Gly Val Leu Tyr Trp Lys Leu Asp Ala
 35 40 45
 Asp Lys Tyr Glu Asn Asp Pro Glu Leu Glu Lys Ile Arg Lys Met Arg
 50 55 60
 Asn Tyr Ser Trp Met Asp Ile Ile Thr Ile Cys Lys Asp Thr Leu Pro
 65 70 75 80
 Asn Tyr Glu Glu Lys Ile Lys Met Phe Phe Glu Glu His Leu His Leu
 85 90 95
 Asp Glu Glu Ile Arg Tyr Ile Leu Glu Gly Ser Gly Tyr Phe Asp Val
 100 105 110
 Arg Asp Lys Glu Asp Lys Trp Ile Arg Ile Ser Met Glu Lys Gly Asp
 115 120 125
 Met Ile Thr Leu Pro Ala Gly Ile Tyr His Arg Phe Thr Leu Asp Glu
 130 135 140
 Lys Asn Tyr Val Lys Ala Met Arg Leu Phe Val Gly Glu Pro Val Trp
 145 150 155 160
 Thr Pro Tyr Asn Arg Pro Ala Asp His Phe Asp Ala Arg Val Gln Tyr
 165 170 175
 Met Ser Phe Leu Glu Gly Thr Ala
 180

<210> 17
 <211> 706
 <212> DNA
 <213> Zebrafish

<220>
 <221> CDS
 <222> (36)..(581)

<400> 17
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 Met Ser Val Phe Glu Ala
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tgg tac atg gat gaa gag tcc gga gag gac cag aga ctc ccg cac aaa	101
Trp Tyr Met Asp Glu Glu Ser Gly Glu Asp Gln Arg Leu Pro His Lys	
10 15 20	
ctg agc ccg aat cag ccc gtc agc gtc cag cag ctg gag cac atc gga	149
Leu Ser Pro Asn Gln Pro Val Ser Val Gln Gln Leu Glu His Ile Gly	
25 30 35	
gtc ttt cac tgg aag ctg aac gct gat atc tat gaa aat gac ccc gaa	197
Val Phe His Trp Lys Leu Asn Ala Asp Ile Tyr Glu Asn Asp Pro Glu	
40 45 50	
ctg cag aag atc cga gag gag aag ggt tat tcc ttt atg gac atc ata	245
Leu Gln Lys Ile Arg Glu Glu Lys Gly Tyr Ser Phe Met Asp Ile Ile	
55 60 65 70	
acc att cac ccg gac aaa ctg ccc gat tac caa aac aaa ctg aaa atg	293
Thr Ile His Pro Asp Lys Leu Pro Asp Tyr Gln Asn Lys Leu Lys Met	
75 80 85	
ttt tac gaa gag cat ctc cac ctg gac gat gag atc cgt tat att ctg	341
Phe Tyr Glu Glu His Leu His Leu Asp Asp Glu Ile Arg Tyr Ile Leu	
90 95 100	
gaa gga tcc tct tat ttt gat gtg cgg gac gaa ggc gac cgc tgg atc	389
Glu Gly Ser Ser Tyr Phe Asp Val Arg Asp Glu Gly Asp Arg Trp Ile	
105 110 115	
cga ata gcg gtg tct aaa ggc gac ctc atc act tta ccg gcc ggg att	437
Arg Ile Ala Val Ser Lys Gly Asp Leu Ile Thr Leu Pro Ala Gly Ile	
120 125 130	
tac cac aga ttc acc gtg gac gaa agc aac tac act aaa gcc atg cgt	485
Tyr His Arg Phe Thr Val Asp Glu Ser Asn Tyr Thr Lys Ala Met Arg	
135 140 145 150	
ctg ttc gtg ggt gaa ccc gtc tgg aag gcc tac aac cgt cca gcc gat	533
Leu Phe Val Gly Glu Pro Val Trp Lys Ala Tyr Asn Arg Pro Ala Asp	
155 160 165	
gac ttt gac atc cgc aag gaa tac gtg aac tcg ctg gga agc tcc tga	581
Asp Phe Asp Ile Arg Lys Glu Tyr Val Asn Ser Leu Gly Ser Ser	
170 175 180	
aatgcctgat gggattgatt tagtgctgag aatcagactc tgcgggtgcct tanacagaca	641
ngcagcaata gtagagctaa catgtcatta cttagtcatc aagacacacc tgatataaag	701

706

<211> 181

<212> PRT

<213> Zebrafish

<400> 18

[illegible]